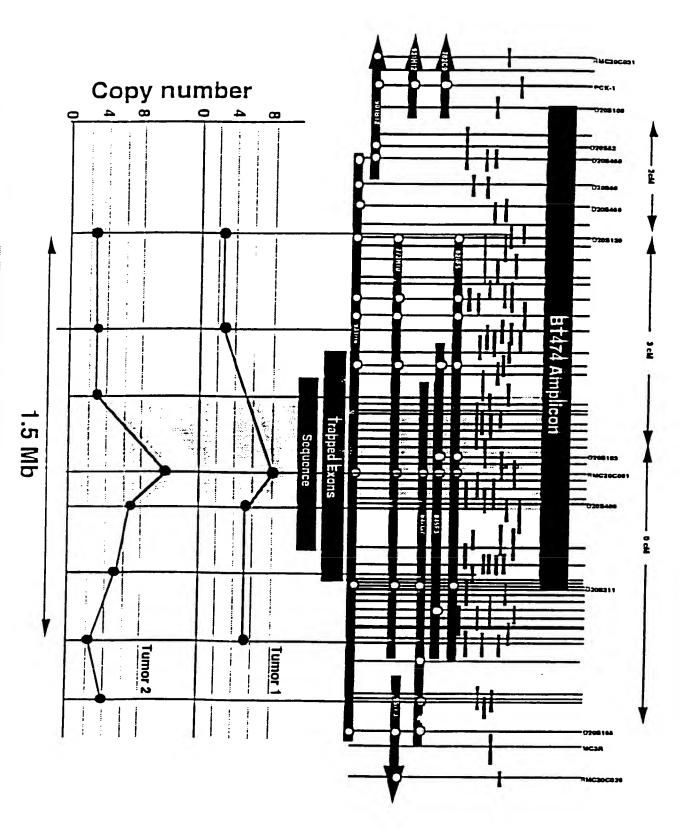


FIGURE 3



And the state of t

ene ID \longrightarrow 1, 2

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4, 5 6, 7, 8, 9, 10, 11

12, 13, 14, 15

, >drell-red TGTGATATTGATTCATGCCCTCTTGCACCTTGCCAAACATCACACGCTTG CCATCCAGTCCACTCGATTTTGGCAGTGCAGATGAAAAACTGGGAACCAT TTGTGTTGAGTCCAGCAAGATGCCAGGACCTGCATGTTTCAGAACGAAGT TCTTCATCATCCAATTTCTCCCTGTATATGGGCTTACCACNACTGCCGTT AAGTCGTGTNAAGTCACCACTCAGGTACATAATGGAATAATTCTGCAAAG GCAGGAGNCACTTTCTCTCCAGTGCTCAGACCATGAAAGTTTTCTGATGT CTTTGGAACTTTGTCTGCAAATAGCTCGAAGGAGACATGGCCTAAAGGCT CGCCATCTGCGGTGATATTGNAACATGGTAGGGCTGACCGTGGCTGTGGC NNNNNNNNNNNNCCCAATGCGGGACAGAGAATCNAAGAAACTGTATTA GGGAAAGGGTCCTGAGTTTATGCCAAAGTTTCCCAGATTGGTTTCCATTG AAACGTAGCTCTGTGAGATACCATCAGGTGTTATGTGAAGAAATGTCTGT GCAAGACTTCCCATCTTCTGTCCCTTTTTATGCTAATGGGTAACACAAAC TCCAAAAGTGGGGTGTACAGCATGAGGCATTAACAAAAATTTATTGGACC CCACACIONNUMNINNUMN

Filtered query sequ

gb|M19533|RATCYCA Rat cyclophilin mRNA, complete cds. Length = 743

Sbjct:

```
Minus Strand HSPs:
Score = 418 (115.5 bits), Expect = 1.5e-58, Sum P(5) = 1.5e-58
Identities = 96/112 (85%), Positives = 96/112 (85%), Strand = Minus /
Plus
Query: 372 TNCAATATCACCGCAGATGGCGAGCCTTTAGGCCATGTCTCCTTCGAGCTATTTGCAGAC
           64 TTCGACATCACGGCTGATGGCGAGCCCTTGGGTCGCGTCTGCTTCGAGCTGTTTGCAGAC
Sbjct:
123
       312 APAGTTCCAAAGACATCAGAAAACTTTCATGGTCTGAGCACTGGAGAAAAG 261
Query:
           124 AAAGTTCCAAAGACAGCAGAAAACTTTCGTGCTCTGAGCACTGGGGAGAAAG 175
Sbjct:
Score = 236 (65.2 bits), Expect = 1.5e-56. Sum P(5) = 1.5e-58
Identities = 52/58 (89%), Positives = 52/58 (89%), Strand = Minus / Plus
       117 TGCTGGACTCAACACAAATGGTTCCCAGTTTTTCATCTGCACTGCCAAAATCGAGTGG 60
Ouerv:
           348 TGCTGGACCAAACACAAATGGTTCCCAGTTTTTTATCTGCACTGCCAAGACTGAGTGG
Sbjct:
405
 Score = 177 (48.9 bits), Expect = 1.5e-58, Sum P(5) = 1.5e-58
 Identities = 41/48 (85%), Positives = 41/48 (65%), Strand = Minus / Plus
         60 GACTGGATGGCAAGCGTGTGATGTTTGGCAAGGTGCAAGAGGGCATGA 13
Query:
           404 GGCTGGATGGCAAGCATGTGGTCTTTGGGAAGGTCAAAGAAGGCATGA 451
Sbict:
 Score = 154 (42.6 bits). Expect = 1.5e-58. Sum P(5) = 1.5e-58
 Identities = 34/38 (89%), Positives = 34/38 (89%), Strand = Minus / Plus
        153 AGAACTTCGTTCTGAAACATGCAGGTCCTGGCATCTTG 116
Query:
           299 AGAACTTCATCCTGAAGCATACAGGTCCTGGCATCTTG 336
Sbjct:
 Score = 85 (23.8 bits), Expect = 1.5e-58, Sum P(5) = 1.5e-58
 Identities = 22/28 (78%), Positives = 22/28 (78%), Strand = Minus / Plus
       256 TOCTGCCTTTGCAGAATTATTCCATTAT 229
Query:
```

Figure 6

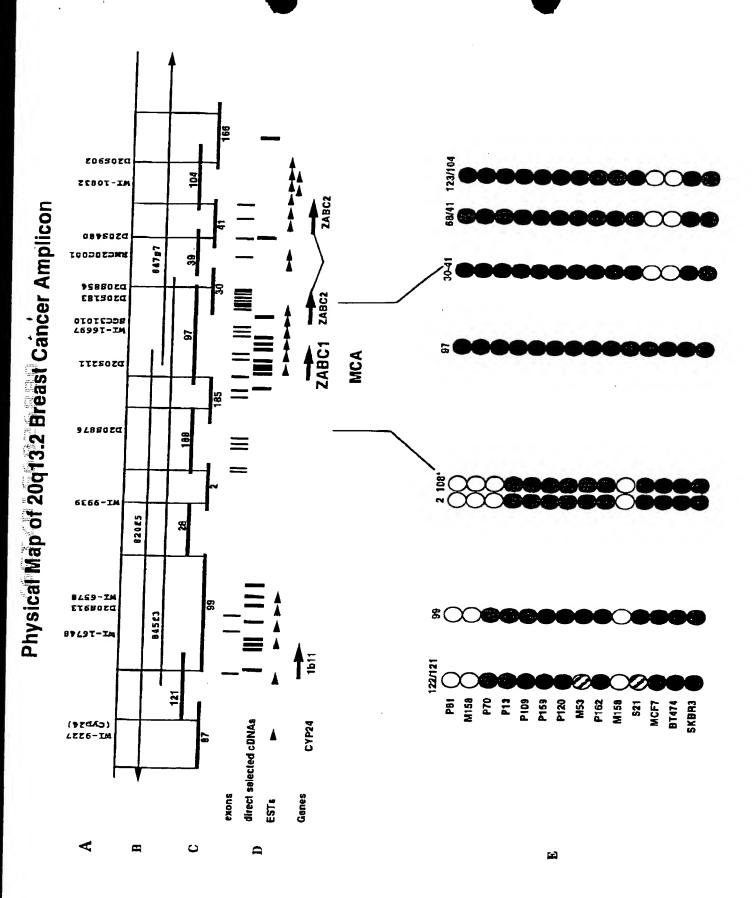


Figure 7